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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:56:54 ; Search time 9.48711 Seconds
(without alignments)
4199.299 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	680.5	96.5	522	3	AAY71312	Aay71312 Rat neuri
2	510	72.3	199	5	ABB81077	Abb81077 Rat neuro
3	503	71.3	118	5	ABB89192	Abb89192 Human pol
4	503	71.3	199	2	AAW53947	Aaw53947 Human NSP
5	503	71.3	199	2	AAW78313	Aaw78313 Fragment
6	503	71.3	199	2	AAW35903	Aay35903 Extended
7	503	71.3	199	3	AAB12805	Aab12805 Human NSP
8	503	71.3	199	4	AAB82348	Aab82348 Human NOG
9	503	71.3	199	5	ABG30939	Abg30939 Human Nog

10	503	71.3	199	5	ABB81080	Abb81080	Human neu
11	499.5	70.9	199	3	AAY71559	Aay71559	Rat Nogo
12	448	63.5	1178	3	AAY71311	Aay71311	Human neu
13	447	63.4	403	3	AAY71563	Aay71563	Rat Nogo
14	447	63.4	893	3	AAY95012	Aay95012	Human sec
15	447	63.4	983	6	ABU11573	Abu11573	Human MDD
16	447	63.4	1162	3	AAY71557	Aay71557	Rat Nogo
17	447	63.4	1163	3	AAY71310	Aay71310	Rat neuro
18	447	63.4	1163	3	AAY71384	Aay71384	Alternati
19	447	63.4	1163	5	ABB81074	Abb81074	Rat neuro
20	447	63.4	1192	3	AAY56967	Aay56967	Human MAG
21	447	63.4	1192	4	AAB82349	Aab82349	Human NOG
22	447	63.4	1192	4	AAU04591	Aau04591	Human Nog
23	447	63.4	1192	5	ABG30938	Abg30938	Human Nog
24	447	63.4	1192	5	ABP68600	Abp68600	Human pan
25	447	63.4	1192	5	ABB81078	Abb81078	Human neu
26	447	63.4	1192	6	ABR59667	Abr59667	Human Nog
27	443	62.8	103	4	AAE03980	Aae03980	Human gen
28	443	62.8	200	4	AAB64514	Aab64514	Human sec
29	443	62.8	359	3	AAY71558	Aay71558	Rat Nogo
30	443	62.8	360	3	AAY71383	Aay71383	Rat neuro
31	443	62.8	360	4	AAE03987	Aae03987	Human gen
32	443	62.8	360	5	ABB81076	Abb81076	Rat neuro
33	443	62.8	361	3	AAY71385	Aay71385	Alternati
34	443	62.8	373	3	AAY53624	Aay53624	A bone ma
35	443	62.8	373	3	AAY56969	Aay56969	Human MAG
36	443	62.8	373	3	AAB24242	Aab24242	Human Nog
37	443	62.8	373	4	AAB82350	Aab82350	Human NOG
38	443	62.8	373	5	AAM47954	Aam47954	Human RTN
39	443	62.8	373	5	ABG30937	Abg30937	Human Nog
40	443	62.8	373	5	ABP68601	Abp68601	Human pan
41	443	62.8	373	5	ABB81079	Abb81079	Human neu
42	443	62.8	379	7	ADB85283	Adb85283	Rat fooce
43	440	62.4	91	2	AAY12360	Aay12360	Human 5'
44	439	62.3	291	4	AAM93484	Aam93484	Human pol
45	410.5	58.2	642	2	AAW58383	Aaw58383	Human sec

ALIGNMENTS

RESULT 1

AAAY71312

ID AAY71312 standard; protein; 522 AA.

XX

AC AAY71312;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo C.

XX

KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region 1. .39

FT /note= "Sequence upstream to the N-terminus of Nogo C

FT protein"

FT Misc-difference 3

FT /note= "Encoded by TAG"

FT Region 11. .191

FT /note= "Region specifically described in claim 16"

FT Misc-difference 29

FT /note= "Encoded by TAA"

FT Protein 40. .238

FT /label= Nogo_C_protein

FT Region 51. .238

FT /note= "C-terminal common region found in Nogo A, B and C

FT isoforms "

FT Region 239. .522

FT /note= "Sequence downstream to the C-terminus of Nogo C

FT protein"

FT Misc-difference 239

FT /note= "Encoded by TGA"

FT Misc-difference 263

FT /note= "Encoded by TGA"

FT Misc-difference 276

FT /note= "Encoded by TAG"

FT Misc-difference 281

FT /note= "Encoded by TGA"

FT Misc-difference 295

FT /note= "Encoded by TAA"

FT Misc-difference 298

FT /note= "Encoded by TAA"

FT Misc-difference 314

FT /note= "Encoded by TGA"

FT Misc-difference 318

FT /note= "Encoded by TGA"

FT Misc-difference 335

FT /note= "Encoded by TAG"

FT Misc-difference 371

FT /note= "Encoded by TGA"

FT Misc-difference 374

FT /note= "Encoded by TAG"

FT Misc-difference 380

FT /note= "Encoded by TAA"

FT Misc-difference 406

FT /note= "Encoded by TAA"

FT Misc-difference 408

FT /note= "Encoded by TAG"

FT Misc-difference 410

FT /note= "Encoded by TAA"

FT Misc-difference 422

FT /note= "Encoded by TAA"

FT Misc-difference 433

FT /note= "Encoded by TGA"

FT Misc-difference 440

FT /note= "Encoded by TAG"
 FT Misc-difference 453
 FT /note= "Encoded by TAG"
 FT Misc-difference 465
 FT /note= "Encoded by TAG"
 FT Misc-difference 482
 FT /note= "Encoded by TAG"
 FT Misc-difference 513
 FT /note= "Encoded by TAA"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 DR N-PSDB; AAD01175.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Claim 7; Fig 14; 122pp; English.
 XX
 CC The present sequence is a rat Nogo C protein which is a potent neural
 CC cell growth inhibitor and is free of all central nervous system (CNS)
 CC myelin material with which it is natively associated. Nogo proteins and
 CC fragments displaying neurite growth inhibitory activity are used in the
 CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
 CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
 CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma,
 CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
 CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
 CC activity can be used to treat or prevent hyperproliferative or benign
 CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
 CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
 CC production of Nogo protein to induce regeneration of neurons or to
 CC promote structural plasticity of the CNS in disorders where neurite
 CC growth, regeneration or maintenance are deficient or desired. The animal
 CC models can be used in diagnostic and screening methods for predisposition
 CC to disorders and to screen for or test molecules which can treat or
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
 CC specification. However the specification does not include sequences for
 CC these SEQ ID numbers
 XX
 SQ Sequence 522 AA;

Query Match 96.5%; Score 680.5; DB 3; Length 522;
 Best Local Similarity 98.6%; Pred. No. 2.5e-71;

Matches 138; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 3 SGEAGVSCLENFAVYSVSVGMHNL-LLLEGRSWQEMDGQKKHWKDKVVDLLYWWDIKKT 61
 |||
 Db 4 SGEAGVSCLENFAVYSVSVGMHNLXLLLEGRSWQEMDGQKKHWKDKVVDLLYWWDIKKT 63

Qy 62 GVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSDEGHPFRAYL 121
 |||
 Db 64 GVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYL 123

Qy 122 ESEVAISEELVQKYSNSALG 141
 |||
 Db 124 ESEVAISEELVQKYSNSALG 143

RESULT 2

ABB81077

ID ABB81077 standard; protein; 199 AA.

XX

AC ABB81077;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-C.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

KW central nervous system; peripheral nervous system; tranquillizer; Nogo;

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;

PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the

PT central/peripheral nervous system from injury/disease, comprises

PT administering nervous system-specific activated T cells/antigen, or

PT analogs/peptides.

XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR N-PSDB; ABL89601.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 11; SEQ ID NO 1568; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 118 AA;

Query Match 71.3%; Score 503; DB 5; Length 118;
Best Local Similarity 98.1%; Pred. No. 3.2e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
|||||:|||||

Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

QY 98 FRIYKGV IQAI AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141

Db 61 FRIYKGV IQAI QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4

AAW53947

ID AAW53947 standard; protein; 199 AA.

XX

AC AAW53947;

XX

DT 24-JUL-1998 (first entry)

XX

DE Human NSPLP protein A.

XX

KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.

XX

OS Homo sapiens.

XX

PN WO9806841-A2.

XX

PD 19-FEB-1998.

XX

PF 24-JUL-1997; 97WO-US013469.

XX

PR 12-AUG-1996; 96US-00700607.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Bandman O, Au-Young J, Goli SK, Hillman J;

XX

DR WPI; 1998-159533/14.

DR N-PSDB; AAV23695.

XX

PT Human neuro-endocrine-specific protein-like proteins - useful for
PT diagnosis, monitoring and treatment of cancer and neuro-degenerative
PT disease.

XX

PS Claim 1; Page 38; 73pp; English.

XX

CC This sequence is a human neuroendocrine-specific protein-like protein
CC (NSPLP) of the invention. Recombinant cells transformed with the DNA are
CC used to express the NSPLP proteins, which are used to treat cancer and
CC neurodegenerative diseases such as amyotrophic lateral sclerosis. Also
CC antisense nucleic acids and antagonists of NSPLP can be used to inhibit
CC activity of the NSPLP proteins. Antibodies specific for NSPLP are used
CC for diagnosis and monitoring treatment of diseases associated with NSPLP
CC expression, in usual immunoassays, and to isolate NSPLP from natural
CC sources. The NSPLP proteins, or their fragments can also be used in drug
CC screening to identify NSPLP antagonists. The nucleic acid can be used
CC diagnostically and for monitoring treatment (in hybridisation or
CC amplification assays); to isolate closely related sequences; in gene
CC therapy for both sense and antisense applications (including use of
CC ribozymes) and for mapping the natural genomic sequence

XX

Query Match 71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 6.4e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 5

ID AAW78313 standard; protein; 199 AA.

AC AAW78313;

DT 13-APR-1999 (first entry)

DE Fragment of human secreted protein encoded by gene 69.

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

PN WO9856804-A1.

PD 17-DEC-1998.

PF 11-JUN-1998; 98WO-US012125.

PR 13-JUN-1997; 97US-0049547P.

PR 13-JUN-1997; 97US-0049549P.

PR 13-JUN-1997; 97US-0049566P.

PB 13-JUN-1997: 97US-0049607P

PR 13-JUN-1997: 97US-0049609P

PR 13-JUN-1997: 97US-0049611P

PR 13-JUN-1997: 97US-0052888B

FR 88 88E 1997, 9785 88519191.

PR 18-AUG-1997; 97US-0055984P.
PR 12-SEP-1997; 97US-0058665P.
PR 12-SEP-1997; 97US-0058668P.
PR 12-SEP-1997; 97US-0058669P.
PR 12-SEP-1997; 97US-0058750P.
PR 12-SEP-1997; 97US-0058971P.
PR 12-SEP-1997; 97US-0058972P.
PR 12-SEP-1997; 97US-0058975P.
PR 02-OCT-1997; 97US-0060834P.
PR 02-OCT-1997; 97US-0060841P.
PR 02-OCT-1997; 97US-0060844P.
PR 02-OCT-1997; 97US-0060865P.
PR 02-OCT-1997; 97US-0061059P.
PR 02-OCT-1997; 97US-0061060P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;
PI Feng P;

XX

DR WPI; 1999-080881/07.

DR N-PSDB; AAX04379.

XX

PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.

XX

PS Disclosure; Page 62; 380pp; English.

XX

CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 86 novel genes and their fragments (nucleic acid sequences:
CC AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 86 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAX04311 for
CC described uses)

XX

SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 2; Length 199;

Best Local Similarity 98.1%; Pred. No. 6.4e-51;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHKWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
|||||:|||||

Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
|||||

RESULT 6

AAY35903

ID AAY35903 standard; protein; 199 AA.

XX

AC AAY35903;

XX

DT 13-SEP-1999 (first entry)

XX

DE Extended human secreted protein sequence, SEQ ID NO. 152.

XX

KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW cellular differentiation; immune system regulator; anti-inflammatory;
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW genetic disease.

XX

OS Homo sapiens.

XX

PN WO9931236-A2.

XX

PD 24-JUN-1999.

XX

PF 17-DEC-1998; 98WO-IB002122.

XX

PR 17-DEC-1997; 97US-0069957P.

PR 09-FEB-1998; 98US-0074121P.

PR 13-APR-1998; 98US-0081563P.

PR 10-AUG-1998; 98US-0096116P.

XX

PA (GEST) GENSET.

XX

PI Bougueleret L, Duclert A, Dumas Milne Edwards J;

XX

DR WPI; 1999-385906/32.

DR N-PSDB; AAX97587.

XX

PT New isolated human secreted proteins.

XX

PS Claim 9; Page 185-186; 516pp; English.

XX

CC This sequence is encoded by an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC act as cytokines or may affect cellular proliferation or differentiation
CC or may act as immune system regulators, haematopoiesis regulators, tissue
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumour inhibition activity. The DNAs can be used in forensic procedures
CC to identify individuals or in diagnostic procedures to identify
CC individuals having genetic diseases resulting from abnormal expression of
CC the genes corresponding to the extended cDNAs. They are also useful for
CC constructing a high resolution map of the human chromosomes. They can
CC also be used for gene therapy to control or treat genetic diseases

XX

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Query Match          71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 6.4e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
             |||||:|||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy          98 FRIYKGV IQAI AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
             |||||:|||||||||||||||||||||||||||||||||||||
Db          61 FRIYKGV IQAI QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

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Query Match 71.3%; Score 503; DB 3; Length 199;
Best Local Similarity 98.1%; Pred. No. 6.4e-51;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 8

ID AAB82348 standard; protein; 199 AA.

AC AAB82348;

DT 23-JUL-2001 (first entry)

DE Human NOGO-C protein.

KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
KW neuromuscular disorder; psychiatric disorder; developmental disorder;
KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
KW cerebroprotective; neuroleptic; diagnosis; therapy.

OS Homo sapiens.

PN WO200136631-A1.

PD 25-MAY-2001.

PF 14-NOV-2000; 2000WO-GB004345.

PR 15-NOV-1999; 99GB-00026995.

XX

XX

PI Michalovich D, Prinjha R;

DR WPI; 2001-343822/36.

XX

PT New polypeptide designated NIGO-C is a splice variant of the human NIGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.

PS Claim 3; Page 25; 25pp; English.

CC The present sequence is that of human NOGO-C, encoded by a novel splice
CC variant of the human NOGO gene on chromosome 2p21. 2 Other splice
CC variants, NOGO-A and NOGO-B, have previously been identified. The
CC invention provides NOGO-C polypeptides and polynucleotides, and methods
CC for producing such polypeptides by recombinant techniques. Also disclosed
CC are methods for utilising NOGO-C polypeptides and polynucleotides in the

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002072493-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-00893348.
 XX
 PR 19-MAY-1998; 98IL-00124500.
 PR 21-JUL-1998; 98WO-US014715.
 PR 22-DEC-1998; 98US-00218277.
 PR 19-MAY-1999; 99US-00314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR N-PSDB; ABN86601.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.
 XX
 PS Example; Page 57-58; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia

RESULT 12
 AAY71311
 ID AAY71311 standard; protein; 1178 AA.
 XX
 AC AAY71311;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Human neurite growth inhibitor Nogo.
 XX
 KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 187
 FT /label= Unknown
 FT Misc-difference 188
 FT /label= Unknown
 FT Misc-difference 189
 FT /label= Unknown
 FT Misc-difference 190
 FT /label= Unknown
 FT Misc-difference 221
 FT /label= Unknown
 FT Misc-difference 328
 FT /label= Unknown
 FT Misc-difference 477
 FT /label= Unknown
 FT Region 977. .1012
 FT /note= "Region specifically described in claim 16"
 FT Region 994. .1174
 FT /note= "Region specifically described in claim 16"
 FT Region 1079. .1114
 FT /note= "Region specifically described in claim 16"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.

XX
 DE Rat Nogo A protein fragment used in the construction of mutant EST.
 XX
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.
 XX
 OS Rattus sp.
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Example; Page; 122pp; English.
 XX
 CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in
 CC the construction of mutant EST. The mutant is composed of His-tag/T7-
 CC tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for
 CC mapping the inhibitory sites of Nogo protein. Major inhibitory region was
 CC identified in the Nogo A sequence from amino acids 172-974, particularly
 CC amino acids 542-722. In addition, N-terminal region 1-171 was found to be
 CC inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is

CC not given in the specification but is derived from rat Nogo A sequence
CC shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC ID NO: 29 in disclosure of the specification. However, the specification
CC does not include sequences for these SEQ ID numbers
XX
SQ Sequence 403 AA;

Query Match 63.4%; Score 447; DB 3; Length 403;
Best Local Similarity 96.9%; Pred. No. 6.9e-44;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db     214 KTSVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 273
        |||||
QY     106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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Db     274 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 309
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RESULT 14

AA95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22 1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX

PF 24-AUG-1999; 99WO-US019351.

XX

PR 24-AUG-1998; 98US-0097638P.

PR 24-AUG-1998; 98US-0097659P.

PR 09-SEP-1998; 98US-0099618P.

PR 28-SEP-1998; 98US-0102092P.

PR 25-NOV-1998; 98US-0109978P.

PR 23-DEC-1998; 98US-0113645P.

PR 23-DEC-1998; 98US-0113646P.

PR 23-AUG-1999; 99US-00379246.

XX

PA (ALPH-) ALPHAGENE INC.

XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US009944.
 XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 DR WPI; 2003-058431/05.
 DR N-PSDB; ABX34563.
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
 XX
 CC This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or

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OM protein - protein search, using sw model

Run on: September 3, 2004, 16:02:30 ; Search time 2.78364 Seconds
(without alignments)
2615.013 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	503	71.3	199	2	US-08-700-607-1	Sequence 1, Appli
2	349	49.5	208	2	US-08-700-607-7	Sequence 7, Appli
3	348	49.4	267	2	US-08-700-607-8	Sequence 8, Appli
4	337	47.8	356	2	US-08-700-607-6	Sequence 6, Appli
5	337	47.8	776	2	US-08-700-607-5	Sequence 5, Appli
6	305	43.3	241	2	US-08-700-607-3	Sequence 3, Appli
7	227	32.2	168	4	US-09-149-476-563	Sequence 563, App
8	99	14.0	80	3	US-08-905-223-411	Sequence 411, App
9	75	10.6	593	4	US-09-328-352-4866	Sequence 4866, Ap
10	72.5	10.3	598	2	US-08-853-659A-53	Sequence 53, Appl
11	71.5	10.1	154	1	US-08-366-783-5	Sequence 5, Appli

12	70	9.9	518	4	US-09-134-001C-4744	Sequence 4744, Ap
13	70	9.9	563	4	US-09-422-936-79	Sequence 79, Appl
14	70	9.9	619	3	US-08-262-220-6	Sequence 6, Appli
15	70	9.9	619	3	US-08-471-733-6	Sequence 6, Appli
16	70	9.9	619	3	US-08-468-878-6	Sequence 6, Appli
17	70	9.9	619	3	US-08-750-494-6	Sequence 6, Appli
18	70	9.9	619	4	US-08-470-638-6	Sequence 6, Appli
19	70	9.9	844	4	US-09-422-936-47	Sequence 47, Appl
20	70	9.9	844	4	US-09-422-936-51	Sequence 51, Appl
21	70	9.9	886	4	US-09-422-936-77	Sequence 77, Appl
22	70	9.9	892	4	US-09-422-936-75	Sequence 75, Appl
23	70	9.9	899	4	US-09-422-936-71	Sequence 71, Appl
24	70	9.9	960	4	US-09-422-936-45	Sequence 45, Appl
25	70	9.9	961	4	US-09-422-936-49	Sequence 49, Appl
26	70	9.9	961	4	US-09-914-259-14	Sequence 14, Appl
27	69	9.8	621	3	US-08-262-220-8	Sequence 8, Appli
28	69	9.8	621	3	US-08-471-733-8	Sequence 8, Appli
29	69	9.8	621	3	US-08-468-878-8	Sequence 8, Appli
30	69	9.8	621	3	US-08-750-494-8	Sequence 8, Appli
31	69	9.8	621	4	US-08-470-638-8	Sequence 8, Appli
32	68	9.6	344	4	US-09-107-532A-6886	Sequence 6886, Ap
33	68	9.6	1447	3	US-09-041-886-25	Sequence 25, Appl
34	68	9.6	1447	5	PCT-US94-05277-2	Sequence 2, Appli
35	67.5	9.6	659	4	US-09-328-352-6021	Sequence 6021, Ap
36	67	9.5	231	4	US-09-198-452A-419	Sequence 419, App
37	67	9.5	493	4	US-09-540-236-2120	Sequence 2120, Ap
38	67	9.5	507	4	US-09-328-352-7742	Sequence 7742, Ap
39	66.5	9.4	249	4	US-09-107-532A-6706	Sequence 6706, Ap
40	66	9.4	445	4	US-09-328-352-4714	Sequence 4714, Ap
41	65.5	9.3	187	2	US-08-846-021A-5	Sequence 5, Appli
42	65.5	9.3	234	1	US-08-366-783-4	Sequence 4, Appli
43	65.5	9.3	254	2	US-08-767-026-7	Sequence 7, Appli
44	65.5	9.3	254	4	US-09-319-275A-7	Sequence 7, Appli
45	65	9.2	424	4	US-09-543-681A-7510	Sequence 7510, Ap

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-1

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Query Match          71.3%; Score 503; DB 2; Length 199;
Best Local Similarity 98.1%; Pred. No. 2.9e-52;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2

US-08-700-607-7

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; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.

```



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; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; LIBRARY: GenBank
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US-08-700-607-8

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Qy      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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RESULT 4

US-08-700-607-6

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; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

```



```

; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; LIBRARY: THP1NOB01
; CLONE: 31870
US-08-700-607-3

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Best Local Similarity 60.9%; Pred. No. 2e-28;
Matches 56; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

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Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
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Db      108 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139

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RESULT 7

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US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06

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; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,637
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; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
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; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          32.2%; Score 227; DB 4; Length 168;
Best Local Similarity 60.0%; Pred. No. 2.7e-19;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
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Qy      71 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQIAIAKSDEGHPFRAYLESEVAISEE 130
          :|||| |::|| :|: ||||| ||||| ||||: ||:||||:||||: :: :| |
Db      1 MLLSLAAFSVISVSVYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy      131 LVQKYSNSAL 140
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Db      61 AFHNYMNAAM 70
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RESULT 8

US-08-905-223-411

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; Sequence 411, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
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; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 411:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -78..-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

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Query Match          14.0%; Score 99; DB 3; Length 80;
Best Local Similarity 58.8%; Pred. No. 0.0002;
Matches 20; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

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Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLS--LTVFSI 80
      | ||::|||:|||| ||| :| :||| |:| |:|
Db      47 VHDLI FWRDVKKTGFVFGTTLIMLLSWQLSVSSV 80

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RESULT 9
US-09-328-352-4866
; Sequence 4866, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4866
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4866

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Query Match          10.6%; Score 75; DB 4; Length 593;
Best Local Similarity 27.5%; Pred. No. 2.5;
Matches 25; Conservative 19; Mismatches 27; Indels 20; Gaps 5;

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Qy 92 --LSVTISFRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
 :||: || : : : | || | ||| :| :: :| |
 Db 209 FIVSIIISLVNHHTNELMKNQKEGQKNRNIFISEVFLSIKMIHTLNNQGL 259

RESULT 11

US-08-366-783-5

; Sequence 5, Application US/08366783

; Patent No. 5650554

; GENERAL INFORMATION:

; APPLICANT: Moloney, Maurice M

; TITLE OF INVENTION: Oil-Body Proteins As Carriers Of

; TITLE OF INVENTION: High-Value Peptides In Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DEHLINGER & ASSOCIATES

; STREET: 350 CAMBRIDGE AVENUE, SUITE 250

; CITY: PALO ALTO

; STATE: California

; COUNTRY: United States

; ZIP: 94025-1536

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/366,783

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: FABIAN, GARY

; REGISTRATION NUMBER: 33,875

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-324-0880

; TELEFAX: 415-324-0960

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 154 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-366-783-5

Query Match 10.1%; Score 71.5; DB 1; Length 154;

Best Local Similarity 26.2%; Pred. No. 1;

Matches 37; Conservative 16; Mismatches 49; Indels 39; Gaps 5;

Qy 33 RSWQEMDGQKKHWKDKVVDLLYWRDIKK--TGVVFGASLFLLSLT----- 76
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Db 6 RDQYQMSGRGSDYSKS-----RQIAKAATAVTAGGSLLVLLSLTLVGTVIALTVATPL 58

Qy 77 --VFSIVSVTAYIALALL-----SVTISFRIYKG-VIAIAKSDEGHPFRAY 120
 :||: | | | :||| ::|: ||| :|: ||: |

Db 59 LVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYLIEHPQGSCLKDSARMK 118


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QY      121 LESEVAISEELVQKYSNSALG 141
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Db      119 LGSKAQDLKDRAQYYGQQHTG 139
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RESULT 12

US-09-134-001C-4744

; Sequence 4744, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

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; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4744

; LENGTH: 518

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; TYPE: PRT
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; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4744

Query Match 9.9%; Score 70; DB 4; Length 518;

Best Local Similarity 21.0%; Pred. No. 8.1;

Matches 21; Conservative 28; Mismatches 35; Indels 16; Gaps 4;

QY 16 AVYSVSVGMH---NLLLLEGRSWQEMDGQKKHKDKVVDLLYWRDIKK---TGVVFGAS 68

Db 400 AIVAITIAWHPNDTILNLVGNAWA---GFGAAFSPLVLYSLYWKDLTRAGAISGMVAGAV 456

Qy 69 LFLLLSLTVFSIVSVTAYIAL-----ALLSVTISFRIYK 102

Db 457 VVIVWISWIKPLATINAFFGMYEIIIPGFIVSVLITYIVSK 496

RESULT 13

US-09-422-936-79

; Sequence 79, Application US/09422936

; Patent No. 6465213

; GENERAL INFORMATION:

; APPLICANT: Ekstrand, Jonas

; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES

; FILE REFERENCE: 06275-165002

; CURRENT APPLICATION NUMBER: US/09/422,936

; CURRENT FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: US 09/242,608

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: PCT/SE98/01947

; PRIOR FILING DATE: 1998-10-27

; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

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; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-422-936-79
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RESULT 14

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; Sequence 6, Application US/08262220
; Patent No. 6054296
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,220
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528

```

; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 619 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-220-6

Query Match 9.9%; Score 70; DB 3; Length 619;
Best Local Similarity 39.0%; Pred. No. 10;
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

QY 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68
| : | : || : | | | | | : || : | |
Db 384 GLAWNKDDGEKESWKVKGSDSYSTRLFGEQDKKSGVALGIS 424

RESULT 15

US-08-471-733-6

; Sequence 6, Application US/08471733
; Patent No. 6068842
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,733
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 619 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-733-6

Query Match 9.9%; Score 70; DB 3; Length 619;
Best Local Similarity 39.0%; Pred. No. 10;
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

Qy 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68
| :| : ||:|: || | | | : ||:| | |
Db 384 GLAWNKDDGEKESWKVKGSDSYSTRLFGEQDKKSGVALGIS 424

Search completed: September 3, 2004, 16:10:40
Job time : 4.78364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2004, 16:00:14 ; Search time 3.01088 Seconds
(without alignments)
4504.667 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	349	49.5	208	2	I60904	neuroendocrine-spe
2	348	49.4	267	2	A60021	tropomyosin-relate
3	337	47.8	776	2	A46583	neuroendocrine-spe
4	162	23.0	2484	2	T26216	hypothetical prote
5	159	22.6	2607	2	T26215	hypothetical prote
6	158	22.4	222	2	T26213	hypothetical prote
7	83.5	11.8	295	2	S59439	probable membrane
8	81.5	11.6	464	2	C88188	protein C18H9.5 [i
9	79	11.2	618	2	T24228	hypothetical prote
10	78.5	11.1	458	2	A72258	hypothetical prote
11	77.5	11.0	261	2	F64924	probable thiosulfa
12	77.5	11.0	583	2	T49359	hypothetical prote
13	76.5	10.9	481	2	C95920	hypothetical membr

14	75.5	10.7	545	2	F64665	glucose-6-phosphat
15	74.5	10.6	545	2	E71851	glucose-6-phosphat
16	74	10.5	268	2	F64024	hypothetical prote
17	73	10.4	393	2	S67763	probable membrane
18	73	10.4	888	2	T01081	hypothetical prote
19	72.5	10.3	278	2	AD0147	probable ABC trans
20	72.5	10.3	302	2	AE2863	conserved hypothet
21	72.5	10.3	302	2	D97640	hypothetical prote
22	72.5	10.3	417	2	B96977	probable Mn transp
23	72.5	10.3	598	2	T14886	leukotoxin express
24	72	10.2	271	2	T13013	hypothetical prote
25	72	10.2	299	2	B69155	hypothetical prote
26	72	10.2	1783	2	T42386	unconventional myo
27	72	10.2	3511	2	A59295	unconventional myo
28	71.5	10.1	255	2	E84899	hypothetical prote
29	71.5	10.1	537	2	G82873	conserved hypothet
30	71	10.1	346	1	WMVZ1W	3beta-hydroxy-Delt
31	71	10.1	346	1	WMVZ2W	3beta-hydroxy-Delt
32	71	10.1	346	2	T37430	hydroxysteroid deh
33	71	10.1	476	2	B97096	2-oxoglutarate/mal
34	71	10.1	1065	2	T25068	hypothetical prote
35	70.5	10.0	153	2	AB3226	conserved hypothet
36	70.5	10.0	261	2	A90926	hypothetical prote
37	70.5	10.0	261	2	E85774	hypothetical prote
38	70.5	10.0	291	2	B69098	phosphate transpor
39	70	9.9	271	2	AC1320	hypothetical prote
40	70	9.9	619	2	S55502	membrane-associate
41	70	9.9	737	2	AE1678	heavy metal-transp
42	69.5	9.9	188	2	T04714	hypothetical prote
43	69.5	9.9	403	2	T04821	hypothetical prote
44	69.5	9.9	415	2	D95248	conserved hypothet
45	69.5	9.9	504	2	E83898	spore germination

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 49.5%; Score 349; DB 2; Length 208;
Best Local Similarity 63.4%; Pred. No. 5.3e-28;
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

```

QY      37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 96
      :||      :|| : :|||||:||||: | || ||| ||:|||| |:||| || ||
Db      9 KMDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATI 68

QY      97 SFRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
      ||||| |:|: |:|||||:|||| |: :|:| :|||:
Db      69 SFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 109

```

RESULT 2

A60021
tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C;Accession: A60021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an
alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 49.4%; Score 348; DB 2; Length 267;
Best Local Similarity 64.0%; Pred. No. 8.9e-28;
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

```

QY      38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
      ||      :|| : : ||||| |||: |||: | || ||| ||: ||| || |||
Db      1 MDCVWSNWKSQAIDLLYWRDIKTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATIS 60

QY      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
      ||||| |:| |:| |||||: ||| |: |:| :|||:
Db      61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 100

```

RESULT 3

A46583
neuroendocrine-specific protein, splice form A - human
N;Contains: neuroendocrine-specific protein, splice form B
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: A46583; I60903
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers,
F.C.; Van de Ven, W.J.
J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 47.8%; Score 337; DB 2; Length 776;
Best Local Similarity 67.4%; Pred. No. 3.7e-26;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
| | :|||||||:|:|:| | | | | | :| | | | | | | | :|
Db 586 KQKAIDLLYWDRDIKTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 645
QY 106 QAIKSDEGHPFRAYLESEVAISEELVQKYSN 137
| | :|:|:|:|:|:| | | :|:|:| | | :|:|:|
Db 646 QAVQKTDEGHPFKAYLELEITLSQEIQKYTD 677

RESULT 4

T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 23.0%; Score 162; DB 2; Length 2484;
Best Local Similarity 31.5%; Pred. No. 7.9e-08;
Matches 34; Conservative 22; Mismatches 48; Indels 4; Gaps 1;

QY 25 HNLLLLLEGRSWQEMDGQKKHWKDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVT 84


```

      |::| | :| : | |::| ||| ||: :| :| :| | : ::|
Db      2269 HSILKHHGDAWIDF----KTVPPCVLDVIYWRDAKKS AIVLSLALLVLFVLAKYPLLT VV 2324

QY      85 AYIALALLSVTISFRIYKGVIAIAKSDEGHPFRAYLESEVAISEELV 132
      | | | |::| | | |::| ||| | :: : :| |
Db      2325 TYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKV 2372

```

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

```

Query Match          22.6%; Score 159; DB 2; Length 2607;
Best Local Similarity 34.5%; Pred. No. 1.7e-07;
Matches 30; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

```

```

QY      46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 105
      | :|::| ||| ||: :| :| :| | : ::| | | | |::| |
Db      2409 KKEVL DVIYWRDAKKS AIVLSLALLVLFVLAKYPLLT VVTYSLLLALGAAAGFRVFKKVE 2468

QY      106 QAIKSDEGHPFRAYLESEVAISEELV 132
      | |:| ||| | :: : :| |
Db      2469 AQIKKTDSEHPFSEILAQDLTLPQEKV 2495

```

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:
A;Gene: CESP:W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 22.4%; Score 158; DB 2; Length 222;
Best Local Similarity 34.1%; Pred. No. 1.4e-08;
Matches 29; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

```
QY      48 KVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 107
          |::|::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      26 KILDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVVTYSLLLALGAAAGFRVFKKVEAQ 85

QY      108 IAKSDEGHPFRAYLESEVAISEELV 132
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      86 IKKTDSEHPFSEILAQDLTLPQEKV 110
```

RESULT 7

S59439

probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein YD9934.17c
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59439
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
A;Molecule type: DNA
A;Residues: 1-295 <MUR>
A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004;
MIPS:YDR233c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 11.8%; Score 83.5; DB 2; Length 295;
Best Local Similarity 26.3%; Pred. No. 0.73;
Matches 25; Conservative 17; Mismatches 32; Indels 21; Gaps 2;

```
QY      41 QKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRI 100
          |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      12 QQQQQKSCNCDLLLWRNPVQTGKYFGGSLALLILKKVNLITFFLKVAYTILFTT----- 66

QY      101 YKGVIAIAKSDEGHPFRAYLESEVAISEELVQKY 135
          | | : : | | | | | | | | | | | | | | | | | | | | | |
Db      67 --GSIEFVSK-----LFLGQGLITKY 85
```

RESULT 8

C88188

protein C18H9.5 [imported] - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C;Accession: C88188
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for
 investigating biology.
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and
 www_sanger.ac.uk/Projects/C_elegans/ for a list of authors
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,
 1999; and Science 285, 1493, 1999
 A;Accession: C88188
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-464 <STO>
 A;Cross-references: GB:chr_II; PID:g722384; GSPDB:GN00020; CESP:C18H9.5
 C;Genetics:
 A;Gene: C18H9.5
 A;Map position: 2

Query Match 11.6%; Score 81.5; DB 2; Length 464;
 Best Local Similarity 25.9%; Pred. No. 1.9;
 Matches 38; Conservative 28; Mismatches 50; Indels 31; Gaps 8;

```

QY      8 VSCLRENFAVYSVSVGMHNLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFG- 66
      ::| | : : :| | : : :| :| : | :| :|
Db     41 ITCTNANMILMNETVICMNDVIEQKSF----SNQTHWLEKSSDISLTFSAAVGAIFGT 96

QY     67 ASLFLLLS-----LTVFSIVSV--TAYIALA----LLSVTISFRIYKGV-----I 105
      | :| | : :| | : | | | :| | :| :| :|
Db     97 VPAVTLISKYGIRKVLTVYGLLSAGGTLMLPLAVNYGLIPVLIA-RLFQGVGASILYSSI 155

QY    106 QAI AKS----DEGHPFRAYLESEVAIS 128
      | :| :| | :| | |
Db    156 GTISESWSPINEIGTFVAFLLSSAFQIS 182
  
```

RESULT 9

T24228

hypothetical protein R166.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T24228

R;Matthews, P.

submitted to the EMBL Data Library, August 1995

A;Reference number: Z19859

A;Accession: T24228

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-618 <WIL>

A;Cross-references: EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:R166.2

A;Experimental source: clone R166

C;Genetics:

A;Gene: CESP:R166.2

A;Map position: 2

Query Match 11.2%; Score 79; DB 2; Length 618;
Best Local Similarity 29.1%; Pred. No. 4.7;
Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;

Query Match 11.1%; Score 78.5; DB 2; Length 458;
Best Local Similarity 26.6%; Pred. No. 3.8;
Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

```

Qy      14 NFAVY-----SVSVGMHNLLLLLEGRSWQEMDGQKKH-----WKD 47
      || :      | : || ||      : ||      ||
Db      196 NFLILSYLRSSIRIGFDFLLL-----TRKHPQLLFIGYFYYSIWIDNFIWKV 244

Qy      48 KVVDLL-----YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR 99
      | ::      | || |      | || | : || || :      | : |
Db      245 KGIEIAPGFFMSPEY--DIPK---FMASLFFIPSLVVFN-----LSMETVVFQR 287

Qy      100 IYKGVIIQAIKSDGHPFRAYLESEVAISEELVQKYSN 137
      |||::| : || : || : | : | : ||
Db      288 NYKGLMQSIV-SDK--PMRVIENLKKLSLSLRHAFSN 322

```

F64924

Query Match 11.0%; Score 77.5; DB 2; Length 261;
Best Local Similarity 27.6%; Pred. No. 2.6;
Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;

```

QY      22 VGMHNLLLLLEGRSWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL----SLT 76
      |:| || | | | |:| : | | |:| :
Db      44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN-----ALLFVLLLASGLIN 94

QY      77 VFSIVSVTAYIALALLSVTISFRI---YKGVIQAIKASDEGHPFR 118
      |:| || |:| : | : : | : | || |:|
Db      95 HFAMVGATAVKSILVAVHEVCGFLLLACWLGFVLINAVGDNGHHYR 139

```

T49359

hypothetical protein B1D1.130 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49359
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.;
Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-583 <SCH>
A;Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:B1D1.130

A;Experimental source: BAC clone B1D1; strain OR74A
C;Genetics:
A;Gene: NCSP:B1D1.130
A;Map position: 6
A;Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;
Best Local Similarity 27.5%; Pred. No. 6.2;
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

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Qy      52 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKS 111
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Db      67 LCYW-PLERRLLVLHALLLLLLLSLEHYS-----AYTRVLLLHITSSNL----- 109

Qy      112 DEGHPFRAYLESEVAIS-----EELVQKYSNSALG 141
          | |  :: || ::      |||:||  |
Db      110 ----PLRVLVDDEV RVAKAIAMAKDINPEELIQKRIEECAG 147
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RESULT 13

C95920

hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021)
megaplasmid pSymB

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: C95920

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Becker, A.; Cowie, A.; Gouzy, J.; Golding, B.; Puhler, A.

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: C95920

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-481 <KUR>

A;Cross-references: GB:AL591985; PIDN:CAC49027.1; PID:g15140512; GSPDB:GN00167

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.; Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.; Huizar, L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Ramsperger, U.; Surzycki, R.; Thebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMb21048

A;Genome: plasmid

Query Match 10.9%; Score 76.5; DB 2; Length 481;
Best Local Similarity 37.7%; Pred. No. 6.4;
Matches 23; Conservative 8; Mismatches 27; Indels 3; Gaps 2;

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Db      238 VYWRKTKSR--VAQALAFLLLVLLLLSTSSV-AYVGLAVLSIPVALSISWSFLSGRMDKD 294

Qy      113 E 113
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Db      295 E 295
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RESULT 14

F64665

glucose-6-phosphate isomerase (EC 5.3.1.9) - *Helicobacter pylori* (strain 26695)

C;Species: *Helicobacter pylori*

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999

C;Accession: F64665

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.;
Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;
Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald,
L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback,
T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.;
Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;
Fraser, C.M.; Venter, J.C.

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: F64665

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-545 <TOM>

A;Cross-references: GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD08211.1;
PID:g2314323; TIGR:HP1166

C;Superfamily: glucose-6-phosphate isomerase

C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 10.7%; Score 75.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 9.2;
Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;

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Db      411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLFKGLDKDEAKDLAHR-----VFFGNRP 464

Qy      70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAIKSD----- 112
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Qy      113 -EGHPFRAYLESEVAISEELVQKYSN 137
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Db      520 LEGHKSNAFDSS---TKHLIELYKN 542
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RESULT 15

E71851

glucose-6-phosphate isomerase - *Helicobacter pylori* (strain J99)

C;Species: *Helicobacter pylori*

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999

C;Accession: E71851

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.;
Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.;
Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen *Helicobacter pylori*.

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: E71851

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-545 <ARN>

A;Cross-references: GB:AE001536; GB:AE001439; NID:g4155675; PIDN:AAD06664.1;
PID:g4155679

A;Experimental source: strain J99

C;Genetics:

A;Gene: *pgi*

C;Superfamily: glucose-6-phosphate isomerase

Query Match 10.6%; Score 74.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

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Db      411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLKGLDKDEAKDLAHR-----VFFGNRP 464

Qy      70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
      :| | | | :| :| | | | | | | | | | | | | | | |
Db      465 SNILLLEKISPSNIGALVALYEHKVFFV----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy      113 -EGHPFRAYLESEVAISEELVQKYSN 137
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Db      520 LEGHKSNAFYDSS---TRHLIELYKN 542

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Search completed: September 3, 2004, 16:10:04

Job time : 8.01088 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2004, 16:09:02 ; Search time 13.9182 Seconds
(without alignments)
3191.803 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	510	72.3	199	9	US-09-893-348-21	Sequence 21, Appl
2	503	71.3	118	15	US-10-264-237-1568	Sequence 1568, Ap
3	503	71.3	199	9	US-09-893-348-25	Sequence 25, Appl
4	503	71.3	199	12	US-10-660-946-1	Sequence 1, Appli
5	503	71.3	199	12	US-09-978-360A-467	Sequence 467, App
6	503	71.3	199	16	US-10-466-258-11	Sequence 11, Appl
7	496	70.4	199	12	US-10-408-967-9	Sequence 9, Appli
8	447	63.4	1163	9	US-09-893-348-18	Sequence 18, Appl
9	447	63.4	1192	9	US-09-789-386-2	Sequence 2, Appli
10	447	63.4	1192	9	US-09-758-140-6	Sequence 6, Appli
11	447	63.4	1192	9	US-09-893-348-23	Sequence 23, Appl
12	447	63.4	1192	9	US-09-972-599A-6	Sequence 6, Appli
13	447	63.4	1192	12	US-10-267-502-429	Sequence 429, App
14	447	63.4	1192	14	US-10-060-036-71	Sequence 71, Appl
15	447	63.4	1192	16	US-10-327-213-9	Sequence 9, Appli
16	447	63.4	1192	16	US-10-466-258-9	Sequence 9, Appli
17	443	62.8	360	9	US-09-893-348-20	Sequence 20, Appl
18	443	62.8	373	9	US-09-789-386-6	Sequence 6, Appli
19	443	62.8	373	9	US-09-765-205-6	Sequence 6, Appli
20	443	62.8	373	9	US-09-893-348-24	Sequence 24, Appl
21	443	62.8	373	12	US-10-408-967-8	Sequence 8, Appli
22	443	62.8	373	14	US-10-060-036-72	Sequence 72, Appl
23	443	62.8	373	16	US-10-466-258-4	Sequence 4, Appli
24	443	62.8	379	14	US-10-205-194-164	Sequence 164, App
25	440	62.4	1192	12	US-10-408-967-7	Sequence 7, Appli
26	436.5	61.9	1163	12	US-10-267-502-431	Sequence 431, App
27	349	49.5	208	12	US-10-660-946-7	Sequence 7, Appli
28	348	49.4	267	12	US-10-660-946-8	Sequence 8, Appli
29	348	49.4	267	14	US-10-205-194-127	Sequence 127, App
30	337	47.8	356	12	US-10-660-946-6	Sequence 6, Appli
31	337	47.8	776	12	US-10-660-946-5	Sequence 5, Appli
32	337	47.8	776	12	US-10-267-502-430	Sequence 430, App
33	337	47.8	777	14	US-10-205-219-93	Sequence 93, Appl
34	337	47.8	780	12	US-10-267-502-432	Sequence 432, App
35	309	43.8	236	9	US-09-729-674-20	Sequence 20, Appl
36	309	43.8	236	9	US-09-765-205-26	Sequence 26, Appl
37	309	43.8	236	12	US-10-408-967-2	Sequence 2, Appli
38	309	43.8	266	12	US-10-276-774-2330	Sequence 2330, Ap
39	309	43.8	269	14	US-10-106-698-6222	Sequence 6222, Ap
40	305	43.3	241	12	US-10-660-946-3	Sequence 3, Appli
41	304	43.1	593	15	US-10-108-260A-2892	Sequence 2892, Ap
42	269	38.2	161	9	US-09-925-302-808	Sequence 808, App
43	269	38.2	161	12	US-09-925-302-808	Sequence 808, App
44	259.5	36.8	204	12	US-10-424-599-194160	Sequence 194160,
45	256	36.3	234	12	US-10-424-599-200840	Sequence 200840,

ALIGNMENTS

RESULT 1
 US-09-893-348-21
 ; Sequence 21, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal

```
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21
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Query Match          72.3%; Score 510; DB 9; Length 199;
Best Local Similarity 99.0%; Pred. No. 5.7e-51;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      38 MDGQKKHKWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Qy      98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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Db      61 FRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
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RESULT 2

US-10-264-237-1568

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; Sequence 1568, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1568
; LENGTH: 118
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (118)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1568

Query Match 71.3%; Score 503; DB 15; Length 118;
Best Local Similarity 98.1%; Pred. No. 1.9e-50;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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Db 61 FRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 3

US-09-893-348-25

; Sequence 25, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-893-348-25

Query Match 71.3%; Score 503; DB 9; Length 199;

Best Local Similarity 98.1%; Pred. No. 3.7e-50;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97

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RESULT 4

US-10-660-946-1

; Sequence 1, Application US/10660946

; Publication No. US20040063131A1

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Au-Young, Janice

; Goli, Surya K.

; Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/660,946

; FILING DATE: 12-Sep-2003

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/228,213A

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/700,607

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 199 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: <Unknown>

; CLONE: Consensus

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:


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Query Match          71.3%;  Score 503;  DB 12;  Length 199;
Best Local Similarity 98.1%;  Pred. No. 3.7e-50;
Matches 102;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy          98 FRIYKGVIIQAIKSDGHPFRAYLESEVAISEELVQKYSNSALG 141
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Query Match          71.3%;   Score 503;   DB 16;   Length 199;
Best Local Similarity 98.1%;   Pred. No. 3.7e-50;
Matches 102;   Conservative      1;   Mismatches      1;   Indels      0;   Gaps      0;

Qy          38 MDGQKKHWKDKVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
             |||||:||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy          98 FRIYKGVIOQIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
             ||||||||||||||||||||
Db          61 FRIYKGVIOQIAQKSDEGHPFRAYLESEVAISEELVOKYSNSALG 104

```

RESULT 7
US-10-408-967-9
; Sequence 9, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng


```

Query Match          63.4%;   Score 447;   DB 9;   Length 1192;
Best Local Similarity 96.9%;   Pred. No. 1.3e-42;
Matches    93;   Conservative    0;   Mismatches    3;   Indels    0;   Gaps    0;

Qy          46 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 105
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1002 KTSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 1061

Qy          106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              ||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

```

```

; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

```

```
Query Match          63.4%; Score 447; DB 9; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.3e-42;  
Matches    93; Conservative      0; Mismatches     3; Indels       0; Gaps        0;
```

```
Qy           46 KDKVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
              | |||  
Db           1002 KTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061
```

```
Qy           106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
              |||
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Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 13

US-10-267-502-429

```
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429
```

Query Match 63.4%; Score 447; DB 12; Length 1192;
Best Local Similarity 96.9%; Pred. No. 1.3e-42;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      46 KDKVVDLLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1002 KTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061

Qy      106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
        ||| | | | | | | | | | | | | | | | | | | | | | |
Db     1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097
```

RESULT 14

US-10-060-036-71

```
; Sequence 71, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
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```

Query Match          63.4%; Score 447; DB 14; Length 1192;
Best Local Similarity 96.9%; Pred. No. 1.3e-42;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          46 KDKVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 105
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1002 KTSVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV I 1061

Qy          106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              | | | | | | | | | | | | | | | | | | | | | |
Db          1062 QAIQKSDEGHPFRAYLESEVAISEELVOKYSNSALG 1097

```

```
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9
```

```

Query Match          63.4%;   Score 447;   DB 16;   Length 1192;
Best Local Similarity 96.9%;   Pred. No. 1.3e-42;
Matches    93;   Conservative    0;   Mismatches    3;   Indels    0;   Gaps    0;

Qy          46 KDKVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 105
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1002 KTSVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1061

Qy          106 QAIKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              | | | | | | | | | | | | | | | | | | | |
Db          1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

```

Search completed: September 3, 2004, 16:30:09
Job time : 14.9182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:59:39 ; Search time 8.86221 Seconds
(without alignments)
5019.975 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLENFVYV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	460	65.2	199	13	Q7T224	Q7t224 gallus gall
2	447	63.4	578	11	Q80W95	Q80w95 mus musculu
3	447	63.4	639	11	Q8K290	Q8k290 mus musculu
4	447	63.4	986	4	Q8IUA4	Q8iua4 homo sapien
5	447	63.4	1046	11	Q8BGK7	Q8bgk7 mus musculu
6	447	63.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
7	443	62.8	356	11	Q8BH78	Q8bh78 mus musculu
8	443	62.8	375	11	Q8BHF5	Q8bhf5 mus musculu
9	443	62.8	392	4	Q96B16	Q96b16 homo sapien
10	436.5	61.9	1163	11	Q8K3G8	Q8k3g8 mus musculu
11	432.5	61.3	357	11	Q8K3G7	Q8k3g7 mus musculu
12	417	59.1	184	6	Q7YRW9	Q7yrw9 bos taurus
13	386	54.8	179	6	Q9GM33	Q9gm33 macaca fasc
14	384	54.5	214	13	Q7T222	Q7t222 carassius a
15	348	49.4	199	4	Q9BQ59	Q9bq59 homo sapien
16	348	49.4	267	11	Q63765	Q63765 rattus sp.
17	337	47.8	780	11	Q8K4S4	Q8k4s4 mus musculu
18	337	47.8	780	11	Q8K0T0	Q8k0t0 mus musculu
19	325	46.1	208	13	Q90637	Q90637 gallus gall
20	320	45.4	760	13	Q90638	Q90638 gallus gall
21	308	43.7	236	11	Q8VBU0	Q8vbu0 rattus norv
22	308	43.7	237	11	Q8C6D5	Q8c6d5 mus musculu
23	308	43.7	643	11	Q8CCU2	Q8ccu2 mus musculu
24	283.5	40.2	221	13	Q7ZUD6	Q7zud6 brachydanio
25	255	36.2	234	5	Q9VMW3	Q9vmw3 drosophila
26	253	35.9	224	5	Q9VMW1	Q9vmw1 drosophila
27	252	35.7	222	5	Q9VMW4	Q9vmw4 drosophila
28	252	35.7	595	5	Q9VMV9	Q9vmv9 drosophila
29	250	35.5	202	5	Q9VMW2	Q9vmw2 drosophila
30	162	23.0	2484	5	Q9U347	Q9u347 caenorhabdi
31	159	22.6	2607	5	Q23187	Q23187 caenorhabdi
32	158	22.4	222	5	Q23188	Q23188 caenorhabdi
33	104	14.8	107	13	Q7T223	Q7t223 carassius a
34	102.5	14.5	154	5	Q9VIB7	Q9vib7 drosophila
35	102.5	14.5	158	5	Q24199	Q24199 drosophila
36	85	12.1	457	10	Q8LDS3	Q8lds3 arabidopsis
37	83.5	11.8	295	3	Q04947	Q04947 saccharomyc
38	82.5	11.7	1247	16	Q88QU8	Q88qu8 pseudomonas
39	81.5	11.6	464	5	Q09484	Q09484 caenorhabdi
40	80	11.3	564	10	Q8L7Z9	Q8l7z9 spinacia ol
41	79	11.2	568	16	Q9CKM1	Q9ckm1 pasteurilla
42	79	11.2	618	5	Q22003	Q22003 caenorhabdi
43	79	11.2	638	16	Q83F64	Q83f64 coxiella bu
44	78.5	11.1	261	16	Q83KX1	Q83kx1 shigella fl
45	78.5	11.1	458	16	Q9X1C8	Q9x1c8 thermotoga

ALIGNMENTS

RESULT 1

Q7T224

ID Q7T224 PRELIMINARY; PRT; 199 AA.
AC Q7T224;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4-C.
 GN RTN4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
 RT RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164737; AAP47312.1; -.
 SQ SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 65.2%; Score 460; DB 13; Length 199;
 Best Local Similarity 88.5%; Pred. No. 6.3e-39;
 Matches 92; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
 ||| |
 Db 1 MDSQPSGWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
 QY 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||||| :||:|:|:|:|:|
 Db 61 FRIYKGVIAIQKSDEGHPFRAYLESDVAVSEDLIQKYSSVVLG 104

RESULT 2

Q80W95

ID Q80W95 PRELIMINARY; PRT; 578 AA.
 AC Q80W95;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nogo-A (Fragment).
 GN NOGO-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tozaki H., Hirata T.;
 RT "The partial sequence of mouse nogo-A cDNA clone#4109.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB073672; BAC75974.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 63.4%; Score 447; DB 11; Length 578;

Best Local Similarity 96.9%; Pred. No. 4.4e-37;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      46 KDKVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
        | |||||||
Db     388 KTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 447

Qy     106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
        ||| |||||||
Db    448 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 483
```

RESULT 3

Q8K290

```

ID      Q8K290          PRELIMINARY;          PRT;      639 AA.
AC      Q8K290;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC032192; AAH32192.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Hypothetical protein.
SQ      SEQUENCE      639 AA;  70312 MW;  309A19DA37603F11 CRC64;

```

Query Match 63.4%; Score 447; DB 11; Length 639;
Best Local Similarity 96.9%; Pred. No. 4.9e-37;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

RESULT 4

Q8 IUA4

```
ID   Q8IUA4          PRELIMINARY;          PRT;    986 AA.
AC   Q8IUA4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
```



```

ID      Q8BGK7          PRELIMINARY;          PRT; 1046 AA.
AC      Q8BGK7;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., Schwab M.E.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7;
RA      Van der Putten H.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129SvcJ7;
RA      Van der Putten H., Mir A.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY102280; AAM73502.1; -.
DR      EMBL; AY102286; AAM73507.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

```

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Qy      46 KDKVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
        | |||||||
Db     856 KTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 915

Qy     106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
        ||| |||||||
Db     916 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 951
```

08BGM9

Query Match 63.4%; Score 447; DB 11; Length 1162;
Best Local Similarity 96.9%; Pred. No. 9.5e-37;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

Q8BH78

Query Match 62.8%; Score 443; DB 11; Length 356;
Best Local Similarity 98.9%; Pred. No. 6.5e-37;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      49  VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
          |||
Db      169 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 228
          |||
Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
          |||
Db      229 OKSDEGHPFRAYLESEVAISEELVQKYSNSALG 261

```

RESULT 8

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.
 AC Q8BHF5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102282; AAM73504.1; -.
 DR EMBL; AY102286; AAM73509.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 375;

Best Local Similarity 98.9%; Pred. No. 6.9e-37;

Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 |||
 Db 188 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 247
 |||
 Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 |||

RESULT 9

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
 AC Q96B16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein (RTN4).
 GN RTN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22376540; PubMed=12488097;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL J. Mol. Biol. 325:299-323(2003).
 DR EMBL; BC016165; AAH16165.1; -.
 DR EMBL; AY102285; AAM64242.1; -.
 DR EMBL; AY102278; AAM64247.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 62.8%; Score 443; DB 4; Length 392;
 Best Local Similarity 98.9%; Pred. No. 7.3e-37;
 Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108

```

      |||
Db      205 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 264
      |||
Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
      |||
Db      265 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 297

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RESULT 10

Q8K3G8

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ID   Q8K3G8          PRELIMINARY;          PRT;   1163 AA.
AC   Q8K3G8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-A.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Long M., Li R., Ju G.;
RT   "Cloning and expression of the mouse Nogo-A protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114152; AAM77068.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;

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Query Match          61.9%;  Score 436.5;  DB 11;  Length 1163;
Best Local Similarity 95.9%;  Pred. No. 1.1e-35;
Matches   93;  Conservative   0;  Mismatches   3;  Indels    1;  Gaps    1;

```

```

Qy      46 KDKVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 104
      | |||
Db      972 KTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1031
      |||
Qy      105 IQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
      |||
Db      1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1068

```

RESULT 11

Q8K3G7

```

ID   Q8K3G7          PRELIMINARY;          PRT;   357 AA.
AC   Q8K3G7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-B.

```


GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jin W., Li R., Long M., Shen J., Ju G.;
 RT "Cloning and expression of the mouse Nogo-B protein."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY114153; AAM77069.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 61.3%; Score 432.5; DB 11; Length 357;
 Best Local Similarity 97.9%; Pred. No. 7.7e-36;
 Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 49 VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 107
 |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
 Db 169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 228
 QY 108 IAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 | ||||||||||||||||||||||||||||||||||||
 Db 229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 262

RESULT 12

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.
 AC Q7YRW9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4w (Fragment).
 GN RTN4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
 RT RTN/Nogo gene family."
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164744; AAP47319.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

Query Match 59.1%; Score 417; DB 6; Length 184;
 Best Local Similarity 96.6%; Pred. No. 1.4e-34;
 Matches 86; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 53 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD 112
 |||
 Db 1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 60
 QY 113 EGHPPFRAYLESEVAISEELVQKYSNSALG 141
 |||
 Db 61 EGHPPFRAYLESEVAISEELVQKYSNSALG 89

RESULT 13

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.
 AC Q9GM33;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB049853; BAB16739.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 54.8%; Score 386; DB 6; Length 179;
 Best Local Similarity 96.4%; Pred. No. 2e-31;
 Matches 81; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 58 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSDEGHPPF 117
 :|||
 Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDDEGHPPF 60
 QY 118 RAYLESEVAISEELVQKYSNSALG 141
 |||
 Db 61 RAYLESEVAISEELVQKYSNSALG 84

RESULT 14

```

ID      Q7T222                PRELIMINARY;          PRT;      214 AA.
AC      Q7T222;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4-M.
GN      RTN4.
OS      Carassius auratus (Goldfish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Carassius.
OX      NCBI_TaxID=7957;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; AY164754; AAP47329.1; -.
SQ      SEQUENCE      214 AA;  24063 MW;  E9B603B043159DD9 CRC64;

```

Qy	43	KHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK	102
		:: ::: : : : :	
Db	21	KHWKEQVVDLLYWRDLQRTGVVFGASLLLLLSLVCSSIISVISYVALALLSVTISFRIYK	80
Qy	103	GVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSAL	140
		:: : :: : : :: ::	
Db	81	GILQAVQKSEDGHPFKMYLDKDIGISSELVQKYSDTAL	118

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ID      Q9BQ59          PRELIMINARY;          PRT;    199 AA.
AC      Q9BQ59;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Similar to reticulon 1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RA      Strausberg R.;
RL      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC003003; AAH03003.1; -.
DR      EMBL; BC000314; AAH00314.1; -.
DR      GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR      GO; GO:0000786; C:nucleosome; IEA.

```

DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
 DR GO; GO:0006334; P:nucleosome assembly; IEA.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 49.4%; Score 348; DB 4; Length 199;
 Best Local Similarity 64.0%; Pred. No. 1.7e-27;
 Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY	38	MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS	97
		: : : : : :	
Db	1	MDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATIS	60
QY	98	FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSN	137
		: : : : : : : : ::	
Db	61	FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD	100

Search completed: September 3, 2004, 16:08:56
 Job time : 11.8622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:58:54 ; Search time 1.8747 Seconds
(without alignments)
3916.307 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match Length DB	ID	Description			
1	495	70.2	199 1	RTN4_MOUSE	Q99p72 mus musculu		
2	447	63.4	1163 1	RTN4_RAT	Q9jk11 rattus norv		
3	447	63.4	1192 1	RTN4_HUMAN	Q9nqc3 homo sapien		
4	337	47.8	776 1	RTN1_HUMAN	Q16799 homo sapien		
5	337	47.8	777 1	RTN1_RAT	Q64548 rattus norv		
6	309	43.8	236 1	RTN3_HUMAN	O95197 homo sapien		
7	308	43.7	237 1	RTN3_MOUSE	Q9es97 mus musculu		
8	214	30.4	545 1	RTN2_HUMAN	O75298 homo sapien		
9	197	27.9	471 1	RTN2_MOUSE	O70622 mus musculu		
10	77.5	11.0	243 1	T2RD_MOUSE	Q9jka2 mus musculu		
11	77.5	11.0	261 1	PHSC_ECOLI	P77409 escherichia		
12	75.5	10.7	246 1	T2R8_MOUSE	Q9jka0 mus musculu		
13	75.5	10.7	545 1	G6PI_HELPY	O25781 helicobacte		
14	74.5	10.6	545 1	G6PI_HELPJ	Q9zk49 helicobacte		
15	74	10.5	268 1	YC73_HAEIN	P44150 haemophilus		
16	72	10.2	614 1	S6AC_RABIT	P48055 oryctolagus		
17	72	10.2	3511 1	MY15_MOUSE	Q9qzz4 mus musculu		

18	71	10.1	346	1	3BHS_VACCC	P21097	v 3 beta-hy
19	71	10.1	346	1	3BHS_VACCV	P26670	v 3 beta-hy
20	70	9.9	960	1	GBR1_MOUSE	Q9wv18	mus musculu
21	70	9.9	961	1	GBR1_HUMAN	Q9ubs5	homo sapien
22	70	9.9	991	1	GBR1_RAT	Q9z0u4	rattus norv
23	69	9.8	315	1	LXD1_PHOLE	P21309	photobacter
24	69	9.8	398	1	PGK_STRPN	Q97s89	streptococc
25	69	9.8	468	1	YDBM_CAEEL	Q19084	caenorhabdi
26	68.5	9.7	238	1	T2RA_MOUSE	Q9jka3	mus musculu
27	68.5	9.7	311	1	HTRB_HAEIN	P45239	haemophilus
28	68.5	9.7	325	1	VP35_VARV	P33059	variola vir
29	68	9.6	184	1	YDB5_SCHPO	Q10358	schizosacch
30	68	9.6	1447	1	DCC_HUMAN	P43146	homo sapien
31	67.5	9.6	324	1	VP35_VACCC	P20497	vaccinia vi
32	67.5	9.6	503	1	LEU1_BUCUM	Q9evh0	buchnera ap
33	67.5	9.6	877	1	SULH_SCHPO	O74377	schizosacch
34	67	9.5	175	1	OLE2_BRANA	P29111	brassica na
35	67	9.5	453	1	SYS_ARCFU	O28244	archaeoglob
36	67	9.5	525	1	SYH_CAEEL	P34183	caenorhabdi
37	67	9.5	756	1	RIR1_HAEIN	P43754	haemophilus
38	66.5	9.4	3174	1	CHAC_HUMAN	Q96rl7	homo sapien
39	66	9.4	253	1	ADH_DROAD	Q00669	drosophila
40	66	9.4	537	1	YCUB_SCHPO	O59831	schizosacch
41	66	9.4	548	1	AMDS_EMENI	P08158	emericeella
42	65.5	9.3	182	1	Y696_METJA	Q58107	methanococc
43	65.5	9.3	398	1	ACK1_NEIMB	Q9jym1	neisseria m
44	65.5	9.3	664	1	NTPI_ENTHR	P43439	enterococcu
45	65.5	9.3	880	1	DPO1_BACSU	O34996	bacillus su

ALIGNMENTS

RESULT 1

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99P72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN RTN4 OR NOGO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RT "Mouse vp20/RTN4C cDNA."
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms may be produced;
 CC Name=1;
 CC IsoId=Q99P72-1; Sequence=Displayed;
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF326337; AAK08076.1; -.
 DR EMBL; AK003859; -; NOT_ANNOTATED_CDS.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 25 CYTOPLASMIC (Potential).

FT TRANSMEM 26 50 POTENTIAL.
 FT DOMAIN 51 137 LUMENAL (Potential).
 FT TRANSMEM 138 162 POTENTIAL.
 FT DOMAIN 163 199 CYTOPLASMIC (Potential).
 FT DOMAIN 12 199 RETICULON.
 SQ SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

Query Match 70.2%; Score 495; DB 1; Length 199;
 Best Local Similarity 97.1%; Pred. No. 2.6e-41;
 Matches 101; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
 || ||| ||||||||||||||||||||||||||||||||||||||||
 Db 1 MDDQKKRWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60
 Qy 98 FRIYKGVIAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
 ||||||||| ||||||||||||||||||||||||||||
 Db 61 FRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 2

RTN4_RAT

ID RTN4 RAT STANDARD; PRT; 1163 AA.
 AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
 DE (Glut4 vesicle 20 kDa protein).
 GN RTN4 OR NOGO.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
 RX MEDLINE=99249816; PubMed=10231557;
 RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
 RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
 RT a new member of the reticulon family."
 RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20129258; PubMed=10667796;
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A.A., Christ F., Schwab M.E.;
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1."
 RL Nature 403:434-439(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

RN [4]
 RP FUNCTION.
 RX MEDLINE=22033691; PubMed=12037567;
 RA GrandPre T., Li S., Strittmatter S.M.;
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
 RL Nature 417:547-551(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF051335; AAF01564.1; -.
 DR EMBL; AJ242961; CAB71027.1; -.
 DR EMBL; AJ242962; CAB71028.1; -.
 DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21010696; PubMed=11126360;
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
 RL Oncogene 19:5736-5746(2000).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20237542; PubMed=10773680;
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
 RT 2p14-->2p13 by radiation hybrid mapping.";
 RL Cytogenet. Cell Genet. 88:101-102(2000).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 4).
 RA Jin W.-L., Ju G.;
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Placenta, and Skeletal muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742;
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.

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DR EMBL; AJ251383; CAB99248.1; -.
 DR EMBL; AJ251384; CAB99249.1; -.
 DR EMBL; AJ251385; CAB99250.1; -.
 DR EMBL; AB040462; BAB18927.1; -.
 DR EMBL; AB040463; BAB18928.1; -.
 DR EMBL; AF148537; AAG12176.1; -.
 DR EMBL; AF148538; AAG12177.1; -.
 DR EMBL; AF087901; AAG12205.1; -.
 DR EMBL; AF320999; AAG40878.1; -.
 DR EMBL; AF132047; AAD31021.1; -.
 DR EMBL; AF132048; AAD31022.1; -.

```

Query Match          63.4%; Score 447; DB 1; Length 1192;
Best Local Similarity 96.9%; Pred. No. 8.4e-36;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          46 KDKVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 105
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          1002 KTSVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1061

Qy          106 QAIKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              | | | | | | | | | | | | | | | | | | | |
Db          1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

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ID      RTN1_HUMAN          STANDARD;          PRT;      776 AA.
AC      Q16799; Q16800; Q16801;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Reticulon 1 (Neuroendocrine-specific protein).
GN      RTN1 OR NSP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC      TISSUE=Lung carcinoma;
RX      MEDLINE=93293865; PubMed=7685762;
RA      Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
RA      Ramaekers F.C.S., Van de Ven W.J.M.;
RT      "Cloning and expression of alternative transcripts of a novel
RT      neuroendocrine-specific gene and identification of its 135-kDa
RT      translational product.";
RL      J. Biol. Chem. 268:13439-13447(1993).
RN      [2]
RP      ALTERNATIVE SPLICING.
RX      MEDLINE=96429995; PubMed=8833145;
RA      Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA      Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT      "Genomic organization of the human NSP gene, prototype of a novel gene
RT      family encoding reticulons.";
RL      Genomics 32:191-199(1996).
RN      [3]
RP      TISSUE SPECIFICITY.
RX      MEDLINE=98228245; PubMed=9560466;
RA      Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA      Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;

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```

RT  "Neuronal differentiation is accompanied by NSP-C expression.";
RL  Cell Tissue Res. 292:229-237(1998).
CC  -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC      membrane trafficking in neuroendocrine cells.
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=RTN1-A; Synonyms=NSP-A;
CC      IsoId=Q16799-1; Sequence=Displayed;
CC      Name=RTN1-B; Synonyms=NSP-B;
CC      IsoId=Q16799-2; Sequence=VSP_005644;
CC      Name=RTN1-C; Synonyms=NSP-C;
CC      IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC  -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC      AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC      IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC  -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
CC  -!- SIMILARITY: Contains 1 reticulon domain.
CC  -----
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CC  -----
DR  EMBL; L10333; AAA59950.1; -.
DR  EMBL; L10334; AAA59951.1; -.
DR  EMBL; L10335; AAA59952.1; -.
DR  PIR; A46583; A46583.
DR  PIR; I60904; I60904.
DR  Genew; HGNC:10467; RTN1.
DR  MIM; 600865; -.
DR  GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
DR  GO; GO:0004871; F:signal transducer activity; NAS.
DR  GO; GO:0030182; P:neuron differentiation; TAS.
DR  GO; GO:0007165; P:signal transduction; NAS.
DR  InterPro; IPR003388; Reticulon.
DR  Pfam; PF02453; Reticulon; 1.
DR  PROSITE; PS50845; RETICULON; 1.
KW  Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW  Phosphorylation.
FT  TRANSMEM      603      623      POTENTIAL.
FT  TRANSMEM      726      746      POTENTIAL.
FT  DOMAIN        589      776      RETICULON.
FT  DOMAIN        609      612      POLY-LEU.
FT  VARSPLIC       1      420      Missing (in isoform RTN1-B).
FT                                     /FTId=VSP_005644.
FT  VARSPLIC       1      568      Missing (in isoform RTN1-C).
FT                                     /FTId=VSP_005645.
FT  VARSPLIC      569      588      GPGPLGPGAPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT                                     KSQ (in isoform RTN1-C).
FT                                     /FTId=VSP_005646.
SQ  SEQUENCE      776 AA;  83617 MW;  CA5B6232353096FE CRC64;

```

Query Match

47.8%; Score 337; DB 1; Length 776;

Best Local Similarity 67.4%; Pred. No. 3e-25;
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY	46	KDKVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI	105
		: : : : :	
Db	586	KQKAIDLlyWRDIKQTGIVFGSfllllfslTQFSVSVVAYLALAALSATISFRIYKSVL	645
QY	106	QAIAKSDEGHPPFRAYLESEVAISEELVQKYSN	137
		: : : : : : : :	
Db	646	QAVQKTDEGHPPKAYLELEITLSQEIQKYTD	677

RESULT 5

```

RTN1_RAT
ID RTN1_RAT STANDARD; PRT; 777 AA.
AC Q64548; Q64547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN RTN1 OR NSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC STRAIN=Wistar; TISSUE=Brain cortex;
RX MEDLINE=96386034; PubMed=8793864;
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA Georgiev G.P., Buchman V.L.;
RT "Intracellular compartmentalization of two differentially spliced s-
RT rex/NSP mRNAs in neurons.";
RL Mol. Cell. Neurosci. 7:289-303(1996).
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC membrane trafficking in neuroendocrine cells.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RTN1-B; Synonyms=S-RexB;
CC IsoId=Q64548-1; Sequence=Displayed;
CC Name=RTN1-S; Synonyms=S-RexS;
CC IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC TYPES.
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC HINDBRAIN.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----

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DR EMBL; U17604; AAC53046.1; -.
 DR EMBL; U17603; AAC53045.1; -.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 604 624 POTENTIAL.
 FT TRANSMEM 727 747 POTENTIAL.
 FT DOMAIN 590 777 RETICULON.
 FT DOMAIN 610 613 POLY-LEU.
 FT VARSPLIC 1 569 Missing (in isoform RTN1-S).
 FT /FTId=VSP_005647.
 FT VARSPLIC 570 589 IPGPLGSDLVPPPLPFFNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-S).
 FT /FTId=VSP_005648.
 SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

Query Match 47.8%; Score 337; DB 1; Length 777;
 Best Local Similarity 67.4%; Pred. No. 3e-25;
 Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 105
 | | :|||||||:|:|:| | | | | | :||| | | :||| | | ||||| | :
 Db 587 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALALAALSATISFRIYKSVL 646
 QY 106 QAIKSDEGHPFRAYLESEVAISEELVQKYSN 137
 ||: |:|||||:|||| | : :|:| :|||:|:
 Db 647 QAVQKTDEGHPFKAYLELEITLSQEIQKYTD 678

RESULT 6

RTN3_HUMAN

ID RTN3_HUMAN STANDARD; PRT; 236 AA.
 AC O95197;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
 DE protein II) (NSPLII).
 GN RTN3 OR NSPL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Retina;
 RX MEDLINE=99265974; PubMed=10331947;
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;

RT "Cloning of a novel member of the reticulon gene family (RTN3): gene
 RT structure and chromosomal localization to 11q13.";
 RL Genomics 58:73-81(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
 RT "Cloning and expression analysis of a cDNA encoding a novel
 RT neuroendocrine-specific protein-like protein 1: NSPL1.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF059524; AAC99319.1; -.
 DR EMBL; AF059529; AAD20951.1; -.
 DR EMBL; AF059525; AAD20951.1; JOINED.
 DR EMBL; AF059526; AAD20951.1; JOINED.
 DR EMBL; AF059527; AAD20951.1; JOINED.
 DR EMBL; AF059528; AAD20951.1; JOINED.
 DR EMBL; AF119297; AAD26810.1; -.
 DR EMBL; BC000634; AAH00634.1; -.
 DR EMBL; BC010556; AAH10556.1; -.

DR EMBL; BC011394; AAH11394.1; -.
 DR EMBL; BC022993; AAH22993.1; -.
 DR Genew; HGNC:10469; RTN3.
 DR MIM; 604249; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT DOMAIN 48 236 RETICULON.
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCDFB7 CRC64;

Query Match 43.8%; Score 309; DB 1; Length 236;
 Best Local Similarity 60.9%; Pred. No. 4.7e-23;
 Matches 56; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 | ||::|||:|||| ||| :| :||| ||::|| :|: ||||| |||||
 Db 48 VHDLIWVRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIAV 107
 QY 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
 ||:|||||:|||: :: :| | | |:|
 Db 108 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139

RESULT 7

RTN3_MOUSE

ID RTN3_MOUSE STANDARD; PRT; 237 AA.
 AC Q9ES97;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 3.
 GN RTN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human
 RT RTN3 homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF195940; AAG31360.1; -.
 DR EMBL; BC014697; AAH14697.1; -.
 DR MGD; MGI:1339970; Rtn3.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 167 187 POTENTIAL.
 FT DOMAIN 49 237 RETICULON.
 SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

Query Match 43.7%; Score 308; DB 1; Length 237;
 Best Local Similarity 59.8%; Pred. No. 6e-23;
 Matches 55; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 108
 | ||::|||:|||| ||| :| :|||| ||::|| :| :|||||||:| ||||:
 Db 49 VHDLI FWRDVKKTGFVFGTTLIMLLSLA AFSVISVSYLILALLSVTISFRVYKSVIAV 108
 Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
 ||:|||||:|||| :: :| | | | :||:
 Db 109 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 140

RESULT 8

RTN2_HUMAN

ID RTN2_HUMAN STANDARD; PRT; 545 AA.
 AC O75298; O60509;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
 DE protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=98360096; PubMed=9693037;
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
 RT "cDNA cloning, genomic organization, and expression of the human RTN2
 RT gene, a member of a gene family encoding reticulons.";
 RL Genomics 51:98-106(1998).
 RN [2]
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
 RC TISSUE=Brain;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression.";
 RL Mamm. Genome 9:274-282(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=RTN2-A;
 CC IsoId=O75298-1; Sequence=Displayed;
 CC Note=Isoform RTN2-C is produced by alternative initiation at
 CC Met-341 of isoform RTN2-A;
 CC Name=RTN2-B;
 CC IsoId=O75298-2; Sequence=VSP_005649;
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
 CC by alternative initiation at Met-1 and Met-341;
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
 CC MUSCLE.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
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 CC -----
 DR EMBL; AF004222; AAC32542.1; -.
 DR EMBL; AF004223; AAC32543.1; -.
 DR EMBL; AF004224; AAC32544.1; -.
 DR EMBL; AF038540; AAC14910.1; -.
 DR Genew; HGNC:10468; RTN2.
 DR MIM; 603183; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0007165; P:signal transduction; NAS.

DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Alternative initiation.
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.
 FT INIT_MET 341 341 FOR ISOFORM RTN2-C.
 FT TRANSMEM 368 388 POTENTIAL.
 FT TRANSMEM 463 483 POTENTIAL.
 FT DOMAIN 345 545 RETICULON.
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).
 FT /FTId=VSP_005649.
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 30.4%; Score 214; DB 1; Length 545;
 Best Local Similarity 46.7%; Pred. No. 2.2e-13;
 Matches 42; Conservative 21; Mismatches 27; Indels 0; Gaps 0;

Qy 48 KVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 107
 || |||||:| : :||| : || | ||||| |:|| || ||| |:|: |:||
 Db 344 KVADLLYWKDTRTSGVVFTGLMVSLLLCLLHFSIVSVA AHLALLLLCGTISLRVYRKVLQA 403
 Qy 108 IAKSDEGHPFRAYLESEVAISEELVQKYSN 137
 : : | :||:|||| : : : : | : : | :
 Db 404 VHRGDGANPFQAYLDVDLTLTREQTERLSH 433

RESULT 9

RTN2_MOUSE

ID RTN2_MOUSE STANDARD; PRT; 471 AA.
 AC 070622; 070620;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression."
 RL Mamm. Genome 9:274-282(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Brain;
 CC IsoId=O70622-1; Sequence=Displayed;
 CC Name=2; Synonyms=Muscle;
 CC IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
 CC tissues.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 DR EMBL; AF038537; AAC14906.1; -.
 DR EMBL; AF038537; AAC14907.1; -.
 DR EMBL; AF038538; AAC14908.1; -.
 DR EMBL; AF038539; AAC14909.1; -.
 DR EMBL; AF093624; AAD13195.1; -.
 DR EMBL; BC031370; AAH31370.1; -.
 DR MGD; MGI:107612; Rtn2.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 295 315 POTENTIAL.
 FT DOMAIN 272 471 RETICULON.
 FT VARSPLIC 1 267 Missing (in isoform 2).
 FT /FTId=VSP_005650.
 FT VARSPLIC 268 271 PLLL -> MGSK (in isoform 2).
 FT /FTId=VSP_005651.
 SQ SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

Query Match 27.9%; Score 197; DB 1; Length 471;

Best Local Similarity 44.3%; Pred. No. 8.6e-12;
Matches 39; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

```

Qy      49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 108
      | |||||:| : :| || : || | ||||| |::|| | || |::| :||:
Db      272 VADLLYWKDTRTSGAVFTGLMASLLCLLHFSIVSVA AHLALLGLCATISLRVYRKVLQAV 331

Qy      109 AKSDEGHPFRAYLESEVAISEELVQKYS 136
      : | :||:||||: :: :: | :: |
Db      332 HRGDGTNPFQAYLDMDLTLTREQTERLS 359

```

RESULT 10

T2RD_MOUSE

```

ID      T2RD_MOUSE      STANDARD;      PRT;      243 AA.
AC      Q9JKA2;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Taste receptor type 2 member 13 (T2R13) (Taste receptor family B
DE      member 3) (TRB3) (Fragment).
GN      TAS2R13.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=DBA/2J;
RX      MEDLINE=20227309; PubMed=10766242;
RA      Matsunami H., Montmayeur J.-P., Buck L.B.;
RT      "A family of candidate taste receptors in human and mouse.";
RL      Nature 404:601-604(2000).
RN      [2]
RP      REVIEW.
RX      MEDLINE=22135574; PubMed=12139982;
RA      Montmayeur J.-P., Matsunami H.;
RT      "Receptors for bitter and sweet taste.";
RL      Curr. Opin. Neurobiol. 12:366-371(2002).
RN      [3]
RP      REVIEW.
RX      MEDLINE=21634924; PubMed=11696554;
RA      Margolskee R.F.;
RT      "Molecular mechanisms of bitter and sweet taste transduction.";
RL      J. Biol. Chem. 277:1-4(2002).
RN      [4]
RP      REVIEW.
RX      MEDLINE=22469025; PubMed=12581520;
RA      Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Cook B., Wu D.,
RA      Zuker C.S., Ryba N.J.;
RT      "Coding of sweet, bitter, and umami tastes: different receptor cells
RT      sharing similar signaling pathways.";
RL      Cell 112:293-301(2003).
CC      -!- FUNCTION: Receptor that may play a role in the perception of
CC      bitterness and is gustducin-linked. May play a role in sensing the
CC      chemical composition of the gastrointestinal content. The activity
CC      of this receptor may stimulate alpha gustducin, mediate PLC-beta-2

```


CC activation and lead to the gating of TRPM5.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
 CC of the tongue and palate epithelium and exclusively in gustducin-
 CC positive cells.
 CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
 CC number of bitter compounds; individual taste cells can
 CC discriminate among bitter stimuli.
 CC -!- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF247733; AAF64510.1; -.
 DR MGD; MGI:1890148; Tas2r13.
 DR InterPro; IPR007960; TAS2R.
 DR Pfam; PF05296; TAS2R; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN <1 12 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 13 33 2 (POTENTIAL).
 FT DOMAIN 34 54 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 55 75 3 (POTENTIAL).
 FT DOMAIN 76 99 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 100 120 4 (POTENTIAL).
 FT DOMAIN 121 150 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 151 171 5 (POTENTIAL).
 FT DOMAIN 172 195 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 196 216 6 (POTENTIAL).
 FT DOMAIN 217 222 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 223 >243 7 (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 243 243
 SQ SEQUENCE 243 AA; 28110 MW; D8AD14AF95B9E0B2 CRC64;

Query Match 11.0%; Score 77.5; DB 1; Length 243;
 Best Local Similarity 27.1%; Pred. No. 2;
 Matches 32; Conservative 18; Mismatches 47; Indels 21; Gaps 5;

Qy 17 VYSVSVGMHNNLLLEGRSWQEMDGQKKH---WKDKVVDLLYWRDIKKTGVVFGASLFLLL 73
 :|| : :|:: || :: | | : : | : | | :|||
 Db 37 LYSALMTTRKVLIIFNNSWTVIN---HFNIWLATCLSIFYFLKIAN---FSNSIFLSL 88
 Qy 74 SLTVFSIVSVTAYIALALLSV-----TISFRIYKGVIAIAKSDEG-HPFRAYL 121
 | :|:||| :| || | || :|| : || | | :|
 Db 89 RWRVKTVVSVTLMMSLLLLLVNVLVINTFIVISVDVYKVNTSYSSHSDNNLHISRIFL 146

RESULT 11
 PHSC_ECOLI
 ID PHSC_ECOLI STANDARD; PRT; 261 AA.
 AC P77409;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE PhsC protein homolog.
 GN YDHU OR B1670.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97175536; PubMed=9023191;
 RA Hensel M., Shea J.E., Bäumler A.J., Gleeson C., Blattner F.R.,
 RA Holden D.W.;
 RT "Analysis of the boundaries of *Salmonella* pathogenicity island 2 and
 RT the corresponding chromosomal region of *Escherichia coli* K-12.";
 RL J. Bacteriol. 179:1105-1111(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Potential).
 CC -!- SIMILARITY: TO *S.TYPHIMURIUM* PHSC.
 CC -----
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 CC -----
 DR EMBL; AE000262; AAC74740.1; -.
 DR EMBL; U68703; AAB47946.1; -.
 DR EMBL; D90810; BAA15442.1; -.

DR PIR; F64924; F64924.
 DR EcoGene; EG13955; ydhU.
 DR InterPro; IPR000516; Ni_hydr_CytB.
 DR Pfam; PF01292; Ni_hydr_CYTB; 1.
 KW Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 108 128 POTENTIAL.
 FT TRANSMEM 182 202 POTENTIAL.
 FT TRANSMEM 224 244 POTENTIAL.
 SQ SEQUENCE 261 AA; 29583 MW; 65CF1A45691A0AF3 CRC64;

Query Match 11.0%; Score 77.5; DB 1; Length 261;
 Best Local Similarity 27.6%; Pred. No. 2.2;
 Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;

Qy 22 VGMHNLLLLLEGRSWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL----SLT 76
 :|:| || | | | : | | | : | | | : | | | :
 Db 44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN-----ALLFVLLLASGLIN 94
 Qy 77 VFSIVSVTAYIALALLSVTISFRI---YKGVIAIAKSDEGHPFR 118
 |:| | | :| : | : | : | : | | | :|
 Db 95 HFAMVGATAVKSLVAVHEVCGFLLLLACWLGFVLINAVGDNGHHYR 139

RESULT 12

T2R8_MOUSE

ID T2R8_MOUSE STANDARD; PRT; 246 AA.
 AC Q9JKA0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Taste receptor type 2 member 8 (T2R8) (Taste receptor family B member
 DE 5) (TRB5) (Fragment).
 GN TAS2R8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20227309; PubMed=10766242;
 RA Matsunami H., Montmayeur J.-P., Buck L.B.;
 RT "A family of candidate taste receptors in human and mouse.";
 RL Nature 404:601-604(2000).
 RN [2]
 RP REVIEW.
 RX MEDLINE=22135574; PubMed=12139982;
 RA Montmayeur J.-P., Matsunami H.;
 RT "Receptors for bitter and sweet taste.";
 RL Curr. Opin. Neurobiol. 12:366-371(2002).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21634924; PubMed=11696554;
 RA Margolskee R.F.;
 RT "Molecular mechanisms of bitter and sweet taste transduction.";

RL J. Biol. Chem. 277:1-4(2002).
 RN [4]
 RP REVIEW.
 RX MEDLINE=22469025; PubMed=12581520;
 RA Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Cook B., Wu D.,
 RA Zuker C.S., Ryba N.J.;
 RT "Coding of sweet, bitter, and umami tastes: different receptor cells
 RT sharing similar signaling pathways.";
 RL Cell 112:293-301(2003).
 CC -!- FUNCTION: Receptor that may play a role in the perception of
 CC bitterness and is gustducin-linked. May play a role in sensing the
 CC chemical composition of the gastrointestinal content. The activity
 CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
 CC activation and lead to the gating of TRPM5.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
 CC of the tongue and palate epithelium and exclusively in gustducin-
 CC positive cells. Expressed in 15% taste bud cells in circumvallate
 CC and foliate papillae but only in 2% in fungiform papillae.
 CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited
 CC number of bitter compounds; individual taste cells can
 CC discriminate among bitter stimuli.
 CC -!- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF247735; AAF64512.1; -.
 DR MGD; MGI:1890259; Tas2r8.
 DR InterPro; IPR007960; TAS2R.
 DR Pfam; PF05296; TAS2R; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 16 36 2 (POTENTIAL).
 FT DOMAIN 37 59 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 60 80 3 (POTENTIAL).
 FT DOMAIN 81 102 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 103 123 4 (POTENTIAL).
 FT DOMAIN 124 153 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 154 174 5 (POTENTIAL).
 FT DOMAIN 175 198 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 199 219 6 (POTENTIAL).
 FT DOMAIN 220 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 246 7 (POTENTIAL).
 FT NON_TER 246 246
 SQ SEQUENCE 246 AA; 28430 MW; 8B8F96F8A62E4474 CRC64;

Query Match 10.7%; Score 75.5; DB 1; Length 246;
 Best Local Similarity 27.1%; Pred. No. 3.3;
 Matches 32; Conservative 18; Mismatches 47; Indels 21; Gaps 5;

CC -!- SIMILARITY: Belongs to the GPI family.
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 CC -----
 DR EMBL; AE001536; AAD06664.1; -.
 DR PIR; E71851; E71851.
 DR HSSP; Q9N1E2; 1HOX.
 DR HAMAP; MF_00473; -; 1.
 DR InterPro; IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; PGI; 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
 FT ACT_SITE 382 382 BY SIMILARITY.
 FT ACT_SITE 510 510 BY SIMILARITY.
 SQ SEQUENCE 545 AA; 62302 MW; 7DB544D95FD1D237 CRC64;

Query Match 10.6%; Score 74.5; DB 1; Length 545;
 Best Local Similarity 25.3%; Pred. No. 9.4;
 Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

Qy 23 GMHNLL-----LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
 | | : | : : : | | : | | : | |
 Db 411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLSSKGLDKDEAKDLAHR-----VFFGNRP 464
 Qy 70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSD----- 112
 : | | | : : | : | | : | | |
 Db 465 SNILLLEKISPSNIGALVALYEHKVFFV----QGVIWDINSFDQWGVELGKELAVPILQE 519
 Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137
 | | | | | : | : | : | |
 Db 520 LEGHKSNAFYDSS---TRHLIELYKN 542

RESULT 15

YC73_HAEIN

ID YC73_HAEIN STANDARD; PRT; 268 AA.
 AC P44150;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein HI1273.
 GN HI1273.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).

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DR EMBL; U32807; AAC22921.1; -.
 DR PIR; F64024; F64024.
 DR TIGR; HI1273; -.
 DR InterPro; IPR000051; SAM_bind.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 268 AA; 30510 MW; E5B28DA7AADC4D0B CRC64;

Query Match 10.5%; Score 74; DB 1; Length 268;
 Best Local Similarity 25.2%; Pred. No. 5;
 Matches 29; Conservative 15; Mismatches 49; Indels 22; Gaps 4;

Qy 8 VSCLRENFAVYSVSVGMHNLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGA 67
 : || | : | : | | | | : : || :
 Db 94 LDCL----AQFKQKFGFLHHLTTFH-----KSWADN-----WDDVPQADVVLAS 132
 Qy 68 SLFLLLSL-TVFSIVSVTAYIALALLSVTISFRIYKGVIAIAKSDEGHPFRAYL 121
 | : | : : | : | || : : || : || : || ||
 Db 133 RSTLVDDLDDMIEKLCAKAKKRVFELTSVTQRHFLDEGVFEAIGREDIGFPTYIYL 187

Search completed: September 3, 2004, 16:06:16
 Job time : 6.8747 secs